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From: Kaufman, Claire  
Sent: Tuesday, November 23, 2004 11:52 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence 09/783,931

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70  
Room: Rem 4E85 Serial #: 09/783,931 Date: 12/23/04

Please search SEQ ID NO: 2, 12, 13, 23 in commercial and interference databases.

Thanks,  
Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

RECEIVED  
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STIC

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:57 ; Search time 40 Seconds  
(without alignments)  
290.141 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	98.9	175	3 US-08-981-392-23	Sequence 23, Appl
2	916	98.9	175	4 US-09-908-322-23	Sequence 23, Appl
3	631.5	68.2	118	3 US-08-981-392-17	Sequence 17, Appl
4	631.5	68.2	118	4 US-09-908-322-17	Sequence 17, Appl
5	527.5	57.0	702	3 US-09-068-740A-4	Sequence 4, Appli
6	527.5	57.0	723	3 US-09-068-740A-9	Sequence 9, Appli
7	527.5	57.0	723	4 US-09-423-753-27	Sequence 27, Appl
8	527.5	57.0	723	4 US-09-641-612-6	Sequence 6, Appli
9	527.5	57.0	723	4 US-10-140-002-346	Sequence 346, App
10	448	48.4	713	3 US-08-872-855-5	Sequence 5, Appli
11	428	46.2	720	3 US-08-872-855-4	Sequence 4, Appli
12	419	45.2	722	3 US-08-981-392-12	Sequence 12, Appl
13	419	45.2	722	4 US-09-908-322-12	Sequence 12, Appl
14	388	41.9	728	3 US-08-981-392-2	Sequence 2, Appli
15	388	41.9	728	4 US-09-908-322-2	Sequence 2, Appli
16	388	41.9	729	3 US-08-872-855-8	Sequence 8, Appli
17	359.5	38.8	187	3 US-08-981-392-46	Sequence 46, Appl
18	359.5	38.8	187	4 US-09-908-322-46	Sequence 46, Appl
19	356	38.4	721	3 US-08-872-855-7	Sequence 7, Appli
20	356	38.4	721	3 US-08-981-392-5	Sequence 5, Appli
21	356	38.4	721	4 US-09-908-322-5	Sequence 5, Appli
22	294.5	31.8	717	3 US-08-872-855-9	Sequence 9, Appli
23	197	21.3	578	3 US-08-981-392-13	Sequence 13, Appl
24	197	21.3	578	4 US-09-908-322-13	Sequence 13, Appl
25	167	18.0	173	3 US-08-981-392-18	Sequence 18, Appl
26	167	18.0	173	4 US-09-908-322-18	Sequence 18, Appl
27	127.5	13.8	685	3 US-08-872-855-2	Sequence 2, Appli

28	127.5	13.8	685	4 US-09-641-612-7	Sequence 7, Appli
29	126.5	13.7	659	4 US-09-423-753-3	Sequence 3, Appli
30	126.5	13.7	685	4 US-09-423-753-25	Sequence 25, Appl
31	126.5	13.7	685	4 US-10-140-002-88	Sequence 88, Appl
32	125	13.5	26	3 US-08-981-392-77	Sequence 77, Appl
33	125	13.5	26	4 US-09-908-322-77	Sequence 77, Appl
34	88.5	9.6	1106	4 US-09-538-092-874	Sequence 874, App
35	82	8.9	407	4 US-09-468-433C-26	Sequence 26, Appl
36	81	8.7	233	4 US-09-311-021-46	Sequence 46, Appl
37	81	8.7	330	4 US-09-252-991A-24637	Sequence 24637, A
38	80.5	8.7	950	4 US-10-009-332-1	Sequence 1, Appli
39	77	8.3	127	4 US-09-489-039A-8856	Sequence 8856, Ap
40	76.5	8.3	874	3 US-09-369-364A-15	Sequence 15, Appl
41	75	8.1	439	4 US-09-724-797-86	Sequence 86, Appl
42	75	8.1	3025	6 5223423-3	Patent No. 5223423
43	74.5	8.0	78	4 US-09-252-991A-19604	Sequence 19604, A
44	74.5	8.0	129	4 US-09-252-991A-16731	Sequence 16731, A
45	74.5	8.0	157	4 US-09-252-991A-31989	Sequence 31989, A

ALIGNMENTS

RESULT 1  
US-08-981-392-23  
; Sequence 23, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-981-392-23

Query Match 98.9%; Score 916; DB 3; Length 175;  
Best Local Similarity 100.0%; Pred. No. 6.3e-97;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423,753
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-27

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

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Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 647 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVVYVISEEKDECVIA 175
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Db 684 -----GEASERKRPDSCGSTSKDTKYQSVVYVISEEKDECVIA 720

RESULT 8
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXFXGDXSSDKNGFQKARYPSVDYNLVQD 60
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Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
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Db 647 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVVYVISEEKDECVIA 175
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RESULT 9
US-10-140-002-346
; Sequence 346, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-346

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXFXGDXSSDKNGFQKARYPSVDYNLVQD 60
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Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 647 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVVYVISEEKDECVIA 175
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Db 684 -----GEASERKRPDSCGSTSKDTKYQSVVYVISEEKDECVIA 720

RESULT 10
US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514



```

; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-5

Query Match 48.4%; Score 448; DB 3; Length 713;
Best Local Similarity 54.3%; Pred. No. 1.6e-42;
Matches 95; Conservative 13; Mismatches 23; Indels 44; Gaps 3;

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Db 580 TMNNLANCQREKDVSVSIIGATQIKNTNKKADF-HGDHGADKSSF-KARYPTVDYNLIRD 637
QY 61 LKGDdTAVRTSHSKRDTKCQSPGSSGRRRPRPHSGXACCGPGSGGTGWVSSWNHCSVS 120
Db 638 LKGDtAVRDAHSKRDTCQSQSAGEEKSTSTLRG----- 673
QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
Db 674 -----GEVDRKRPEVSYSTSKDTKYQSVYVLSAEKDECVIA 710

RESULT 11
US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-872-855-4

Query Match 46.2%; Score 428; DB 3; Length 720;
Best Local Similarity 53.7%; Pred. No. 3.1e-40;
Matches 94; Conservative 12; Mismatches 25; Indels 44; Gaps 4;

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Db 587 TMNNLANCQREKDVSVSIIGATQIKNTNKKADF-HGDHGAKKSSF-KVRYPTVDYNLVRD 644
QY 61 LKGDdTAVRTSHSKRDTKCQSPGSSGRRRPRPHSGXACCGPGSGGTGWVSSWNHCSVS 120
Db 645 LKGDtAVRDTSHSKRDTKCQSQSAGEEK-----IAPTLRG----- 680
QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
Db 681 -----GEIPDRKRPEVSYSTSKDTKYQSVYVLSAEKDECVIA 717

RESULT 12
US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-981-392-12

Query Match 45.2%; Score 419; DB 3; Length 722;
Best Local Similarity 52.6%; Pred. No. 3.3e-39;
Matches 92; Conservative 12; Mismatches 27; Indels 44; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGXGSDXSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCQREKDVSVSIIGATQIKNTNKKADF-HGDHGAEEKSSF-KVRYPTVDYNLVRD 646

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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:12 ; Search time 194 Seconds  
(without alignments)  
519.024 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926  
Sequence: 1 TMNLANCOREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	527.5	57.0	723	1	DLL1_HUMAN	O00548 homo sapien
2	445	48.1	714	1	DLL1_RAT	P97677 rattus norv
3	431	46.5	722	2	Q6PFV7	Q6pfv7 mus musculu
4	431	46.5	722	2	AAH57400	Aah57400 mus muscu
5	431	46.5	722	2	AAR30869	Aar30869 mus muscu
6	431	46.5	722	2	AAH65063	Aah65063 mus muscu
7	428	46.2	722	1	DLL1_MOUSE	Q61483 mus musculu
8	388	41.9	728	2	Q90656	Q90656 gallus gall
9	387.5	41.8	726	2	Q8AW87	Q8aw87 cynops pyrr
10	356	38.4	721	2	Q91902	Q91902 xenopus lae
11	294.5	31.8	717	2	P87357	P87357 brachydanio
12	294.5	31.8	720	2	Q8UWJ4	Q8uwj4 brachydanio
13	218	23.5	772	2	Q6DI48	Q6di48 brachydanio
14	149	16.1	802	2	O57462	O57462 brachydanio
15	126.5	13.7	685	1	DLL4_HUMAN	Q9nr61 homo sapien
16	126.5	13.7	686	1	DLL4_MOUSE	Q9ji71 mus musculu
17	125.5	13.6	686	2	Q9DBU9	Q9dbu9 mus musculu
18	91	9.8	364	2	Q6MZM8	Q6mzm8 homo sapien
19	91	9.8	364	2	Q6N000	Q6n000 homo sapien
20	91	9.8	364	2	CAE45875	Cae45875 homo sapi
21	91	9.8	364	2	CAE45984	Cae45984 homo sapi
22	91	9.8	364	2	CAE46001	Cae46001 homo sapi
23	88.5	9.6	1106	1	GLI1_HUMAN	P08151 homo sapien
24	87.5	9.4	906	2	Q8I7K4	Q8i7k4 caenorhabdi
25	87.5	9.4	1837	2	Q95ZU1	Q95zul caenorhabdi
26	87.5	9.4	1839	2	Q17383	Q17383 caenorhabdi
27	86.5	9.3	167	2	Q8CEA2	Q8cea2 mus musculu
28	86.5	9.3	845	2	Q6XGW8	Q6xgw8 hepatitis b
29	86.5	9.3	845	2	AAP79719	Aap79719 hepatitis
30	86.5	9.3	1561	1	Y34F_DROME	Q9w5d0 drosophila
31	84.5	9.1	845	2	Q6XGM0	Q6xgm0 hepatitis b

32	84.5	9.1	845	2	Q6XGR9	Q6xgr9 hepatitis b
33	84.5	9.1	845	2	AAP79768	Aap79768 hepatitis
34	84.5	9.1	845	2	AAP79817	Aap79817 hepatitis
35	84	9.1	407	1	MGB6_HUMAN	Q8n7x4 homo sapien
36	84	9.1	541	2	Q86UZ3	Q86uz3 homo sapien
37	83.5	9.0	1651	1	ROB1_RAT	O55005 rattus norv
38	83	9.0	438	2	Q6ZDE6	Q6zde6 oryza sativ
39	83	9.0	438	2	BAD09364	Bad09364 oryza sat
40	83	9.0	657	2	Q8JXJ8	Q8jxj8 hepatitis b
41	83	9.0	1694	2	Q17652	Q17652 caenorhabdi
42	82.5	8.9	845	2	Q6XGR2	Q6xgr2 hepatitis b
43	82.5	8.9	845	2	AAP79775	Aap79775 hepatitis
44	82.5	8.9	1431	1	CA1G_MESAU	Q9jmh4 mesocricetu
45	82	8.9	311	2	Q8H077	Q8h077 oryza sativ

ALIGNMENTS

RESULT 1

ID	DLL1_HUMAN	STANDARD;	PRT;	723 AA.
AC	O00548; Q9NU41; Q9UJV2;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal)			
DE	(H-Delta-1) (UNQ146/PRO172).			
GN	Name=DLL1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99180765; PubMed=10079256;			
RA	Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,			
RA	Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;			
RT	"Human ligands of the Notch receptor.";			
RL	Am. J. Pathol. 154:785-794(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han W., Ye Q., Moore M.A.S.;			
RT	"A soluble form of human delta-like-1 inhibits differentiation of			
RT	hematopoietic progenitor cells.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Oda T., Chandrasekharappa S.C.;			
RT	"Human Delta 1 gene sequence.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandien R., Watanabe C., Wiewand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Almeida J.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.			
RN	[6]			
RP	FUNCTION.			

RX MEDLINE=21464863; PubMed=11581320;  
RA Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,  
RA Henrique D., Parreira L.;  
RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human  
lymphoid differentiation.";  
RL J. Exp. Med. 194:991-1001(2001).  
CC -!- FUNCTION: Acts as a ligand for Notch receptors. Blocks the  
differentiation of progenitor cells into the B-cell lineage while  
promoting the emergence of a population of cells with the  
characteristics of a T-cell/NK-cell precursor.  
CC -!- SUBUNIT: Interacts with Notch receptors.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower  
expression in brain and muscle and almost no expression in  
placenta, lung, liver, and kidney.  
CC -!- SIMILARITY: Contains 1 DSL domain.  
CC -!- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF003522; AAB61286.1; -.  
DR EMBL; AF196571; AAF05834.1; -.  
DR EMBL; AF222310; AAG09716.1; -.  
DR EMBL; AY358892; AAQ89251.1; -.  
DR EMBL; AL078605; CAB89569.1; -.  
DR HSSP; P00740; 1EDM.  
DR Genew; HGNC:2908; DLL1.  
DR MIM; 606582; -.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005112; F:Notch binding; IPI.  
DR GO; GO:0030154; P:cell differentiation; TAS.  
DR GO; GO:0001709; P:cell fate determination; NAS.  
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.  
DR GO; GO:0009912; P:hair cell fate commitment; ISS.  
DR GO; GO:0030097; P:hemoipoiesis; NAS.  
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.  
DR GO; GO:0007399; P:neurogenesis; ISS.  
DR GO; GO:0007219; P:Notch signaling pathway; NAS.  
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.  
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.  
DR InterPro; IPR00152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 7.  
DR PROSITE; PS01187; EGF\_CA; 1.  
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
KW Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 723 Delta-like protein 1.  
FT DOMAIN 18 545 Extracellular (Potential).  
FT TRANSMEM 546 568 Potential.  
FT DOMAIN 569 723 Cytoplasmic (Potential).  
FT DOMAIN 159 221 DSL.  
FT DOMAIN 226 254 EGF-like 1.  
FT DOMAIN 257 285 EGF-like 2.

FT DOMAIN 292 325 EGF-like 3.  
FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).  
FT DOMAIN 370 402 EGF-like 5.  
FT DOMAIN 409 440 EGF-like 6.  
FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).  
FT DOMAIN 485 516 EGF-like 8.  
FT DISULFID 226 237 By similarity.  
FT DISULFID 230 243 By similarity.  
FT DISULFID 245 254 By similarity.  
FT DISULFID 257 268 By similarity.  
FT DISULFID 263 274 By similarity.  
FT DISULFID 276 285 By similarity.  
FT DISULFID 292 304 By similarity.  
FT DISULFID 298 314 By similarity.  
FT DISULFID 316 325 By similarity.  
FT DISULFID 332 343 By similarity.  
FT DISULFID 337 352 By similarity.  
FT DISULFID 354 363 By similarity.  
FT DISULFID 370 381 By similarity.  
FT DISULFID 375 391 By similarity.  
FT DISULFID 393 402 By similarity.  
FT DISULFID 409 420 By similarity.  
FT DISULFID 414 429 By similarity.  
FT DISULFID 431 440 By similarity.  
FT DISULFID 447 467 By similarity.  
FT DISULFID 469 478 By similarity.  
FT DISULFID 485 496 By similarity.  
FT DISULFID 490 505 By similarity.  
FT DISULFID 507 516 By similarity.  
FT CARBOHYD 477 477 N-linked (GlcNAc... ) (Potential).  
FT CONFLICT 498 498 E -> Q (in Ref. 2).  
FT CONFLICT 502 502 G -> R (in Ref. 4 and 5).  
FT CONFLICT 510 510 G -> S (in Ref. 2).  
SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;  
  
Query Match 57.0%; Score 527.5; DB 1; Length 723;  
Best Local Similarity 64.8%; Pred. No. 2.7e-43;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
  
QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGXSDKNGFQKARYPSVDYNLVQD 60  
Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDSADKNGF-KARYPAVDYNLVQD 646  
  
QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWSSWNHCSV 119  
Db 647 LKGGDDTAVRDAHSHSKRDTKCQPGSSGEEKGPTTLRG----- 683  
  
QY 120 SLPKCSHAFIVDFLYFFPSGEASERKRPDPSGCSTSKDTKYQSVVYVISEEKDECVIA 175  
Db 684 -----GEASERKRPDPSGCSTSKDTKYQSVVYVISEEKDECVIA 720  
  
RESULT 2  
DLL1 RAT  
ID \_DLL1 RAT STANDARD; PRT; 714 AA.  
AC P97677;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).  
GN Name=Dll1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Disibio G., Hebshi L., Boulter J., Weinmaster G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May be involved in cell-to-cell communication in  
mammalian embryos. May have a role in cellular interactions  
underlying somitogenesis and development of the nervous system (By  
similarity).  
CC











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OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura K., Kikuchi Y., Sueaki K., Chiba C., Saito T.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AB095017; BAC41350.2; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 6.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 726 AA; 79866 MW; 352A40219AE67F41 CRC64;

Query Match 41.8%; Score 387.5; DB 2; Length 726;
Best Local Similarity 50.3%; Pred. No. 1.8e-29;
Matches 88; Conservative 17; Mismatches 25; Indels 45; Gaps 5;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGXSSDKNGFQKARYPSVDYNLVQD 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
594 TMNNLANCRRKDISVSVIGATQIKNTNKKADL-YSESTSDKNGY-KARYPSVDYNLVHE 651
QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGTGWGVSSWNHCSVS 120
Db ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
652 LKHED-SVKEEHGKRESKCIANGSEADEKHP-----VQ 683

QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEKDECVIA 175
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
684 LK-----SSETSERRRPESLYSTSKETKYQSVYVISEAKDECIIA 723

RESULT 10
Q91902 PRELIMINARY; PRT; 721 AA.
ID Q91902
AC Q91902;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
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RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
RT the Drosophila neurogenic gene Delta.";
RL Nature 375:761-766(1995).
DR EMBL; L42229; AAC38017.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;

Query Match 38.4%; Score 356; DB 2; Length 721;
Best Local Similarity 46.3%; Pred. No. 2.3e-26;
Matches 81; Conservative 15; Mismatches 33; Indels 46; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGXSSDKNGFQKARYPSVDYNLVQD 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
590 TMNNLANCQREKDISVFIGTQIKNTNKKIDF-LSESNNEKNGY-KPRYPSPVDYNLVHE 647
QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGTGWGVSSWNHCSVS 120
Db ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
648 LKNEDSP-KEERSKCEAKCSSNDSSE----- 673

QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEKDECVIA 175
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
674 -----DVNSVHVKRDSERRRPDSAYSTSKDTKYQSVYVISDEKDECIIA 718

RESULT 11
P87357 PRELIMINARY; PRT; 717 AA.
ID P87357
AC P87357;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DeltaD transmembrane protein precursor.
GN Name=dld; Synonyms=deltaD;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97346722; PubMed=9203139;
RA Dornseifer P., Takke C., Campos-Ortega J.A.;
RT "Overexpression of a zebrafish homologue of the Drosophila neurogenic
RT gene delta perturbs differentiation of primary neurons and somitic
RT development.";
RL Mech. Dev. 63:159-171(1997).
DR EMBL; Y11760; CAA72425.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-990415-47; dld.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
```



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DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain; Signal; Transmembrane.
KW EGF-like domain; Signal; Transmembrane.
FT SIGNAL 4 11 Potential.
SQ SEQUENCE 717 AA; 79061 MW; 9C5A0162504593E4 CRC64;

Query Match 31.8%; Score 294.5; DB 2; Length 717;
Best Local Similarity 42.0%; Pred. No. 2.7e-20;
Matches 74; Conservative 14; Mismatches 37; Indels 51; Gaps 7;

QY 1 TMNNLANCQ-REKDISVSIIGATGIXNTNKKADFXDXGDSXSDKNGFQKARYPSVDYNLVQ 59
||||| : ||||:||||||| : ||||| ||||| :|| |||||
Db 589 TMNLTNRSREKDLVSIIGATQVKNINKVDF--QSDGDKNGF-KSRYSLVDYNLVH 644
||||| : ||||:||||||| : ||||| ||||| :|| |||||

QY 60 DLKGGDDTAVRTSHSKRDTKCQSPGSSGRRRGRPRPHSGXACCGPGSGGTGWVSSWNHCSV 119
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 645 ELKQEDLGKEDSERSEATKCEPLDSDSEK-----HR-----NH--- 678
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTS KDTKYQSVYVISEEKDECVIA 175
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 679 -----LKSDSSERKRTESLC---KDTKYQSVFVLSEKDECIIA 714
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 12
Q8UWJ4
ID Q8UWJ4 PRELIMINARY; PRT; 720 AA.
AC Q8UWJ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DeltaD protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22248969; PubMed=12361969;
RA Hans S., Campos-Ortega J.A.;
RT "On the organisation of the regulatory region of the zebrafish deltaD
gene.";
RL Development 129:4773-4784(2002).
DR EMBL; AF426384; AAL31528.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
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DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 720 AA; 79380 MW; DE6B7393E2AA0FE6 CRC64;

Query Match 31.8%; Score 294.5; DB 2; Length 720;
Best Local Similarity 42.0%; Pred. No. 2.7e-20;
Matches 74; Conservative 14; Mismatches 37; Indels 51; Gaps 7;

QY 1 TMNNLANCQ-REKDISVSIIGATGIXNTNKKADFXDXGDSXSDKNGFQKARYPSVDYNLVQ 59
||||| : ||||:||||||| : ||||| ||||| :|| |||||
Db 589 TMNLTNRSREKDLVSIIGATQVKNINKVDF--QSDGDKNGF-KSRYSLVDYNLVH 644
||||| : ||||:||||||| : ||||| ||||| :|| |||||

QY 60 DLKGGDDTAVRTSHSKRDTKCQSPGSSGRRRGRPRPHSGXACCGPGSGGTGWVSSWNHCSV 119
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 645 ELKQEDLGKEDSERSEATKCEPLDSDSEK-----HR-----NH--- 678
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTS KDTKYQSVYVISEEKDECVIA 175
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 679 -----LKSDSSERKRTESLC---KDTKYQSVFVLSEKDECIIA 714
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 13
Q6DI48
ID Q6DI48 PRELIMINARY; PRT; 772 AA.
AC Q6DI48;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075742; AAH75742.1; -.
KW Hypothetical protein.
SQ SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;

Query Match 23.5%; Score 218; DB 2; Length 772;
Best Local Similarity 35.0%; Pred. No. 1.1e-12;
Matches 70; Conservative 24; Mismatches 70; Indels 36; Gaps 9;
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CC -!- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF253468; AAF76427.1; -.  
DR EMBL; AB036931; BAB16085.1; -.  
DR EMBL; AB043894; BAB18581.1; -.  
DR EMBL; AY358894; AAQ89253.1; -.  
DR EMBL; AF279305; AAF81912.1; -.  
DR PIR; JC7570; JC7570.  
DR HSSP; P00740; 1EDM.  
DR Genew; HGNC:2910; DLL4.  
DR MIM; 605185; -.  
DR GO; GO:0005112; F:Notch binding; TAS.  
DR GO; GO:0008015; P:circulation; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 7.  
DR PRINTS; PR00010; EGFBL00D.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 8.  
KW Developmental protein; Differentiation; Direct protein sequencing;  
KW EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 26  
FT CHAIN 27 685 Delta-like protein 4.  
FT DOMAIN 27 529 Extracellular (Potential).  
FT TRANSMEM 530 550 Potential.  
FT DOMAIN 551 685 Cytoplasmic (Potential).  
FT DOMAIN 155 217 DSL.  
FT DOMAIN 218 251 EGF-like 1.  
FT DOMAIN 252 282 EGF-like 2.  
FT DOMAIN 284 322 EGF-like 3.  
FT DOMAIN 324 360 EGF-like 4.  
FT DOMAIN 362 400 EGF-like 5.  
FT DOMAIN 402 438 EGF-like 6.  
FT DOMAIN 440 476 EGF-like 7.  
FT DOMAIN 480 518 EGF-like 8.  
FT DISULFID 222 233 By similarity.  
FT DISULFID 226 239 By similarity.  
FT DISULFID 241 250 By similarity.  
FT DISULFID 253 264 By similarity.  
FT DISULFID 259 270 By similarity.  
FT DISULFID 272 281 By similarity.  
FT DISULFID 288 300 By similarity.  
FT DISULFID 294 310 By similarity.  
FT DISULFID 312 321 By similarity.  
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FT DISULFID 350 359 By similarity.  
FT DISULFID 366 377 By similarity.  
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FT DISULFID 390 399 By similarity.  
FT DISULFID 406 417 By similarity.  
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FT DISULFID 444 464 By similarity.  
FT DISULFID 466 475 By similarity.  
FT DISULFID 484 495 By similarity.  
FT DISULFID 489 506 By similarity.  
FT DISULFID 508 517 By similarity.

FT	CARBOHYD	108	108	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	183	183	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	205	205	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	393	393	N-linked (GlcNAc. . .)	(Potential).
SQ	SEQUENCE	685 AA;	74604 MW;	6CF89D3C220ACC89	CRC64;

Query Match 13.7%; Score 126.5; DB 1; Length 685;  
Best Local Similarity 26.7%; Pred. No. 0.001;  
Matches 47; Conservative 23; Mismatches 43; Indels 63; Gaps 7;

Qy	2	MNNLANCQREKD	ISVSIIGATGIXNTNKKAD	FXXXGDXSSDKNGFQKARYPSVDY	NLVQDL 61
Db	568	MNNLSDFQKD	-----NLIPAAQLKNTNQK	KELEV-DCGLDKSNCGKQQNHTLDY	NL----- 617
Qy	62	KGDDTAVRTSH	KRDTKCQSPGSSGR--RRGPR	PHSGXACCGPGSGGTWGVSSWNH	CSV 119
Db	618	-----	-----APGLGRGTMPGK	FPHSDKSL-----GEKAPLR	LHS 648
Qy	120	SLPKCSHAFIV	DFLYFPFSGEASERKRPD	SGCSTSKDTKYQSVVYVISEEK	DECVIA 175
Db	649	EXPEC-----	-----RISAICS-PRDS	MYQSVCLISEERNECVIA	682

Search completed: December 2, 2004, 04:01:22  
Job time : 196 secs



A;Residues: 1-728 <HEN>  
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:9882411; PIDN:AAC59689.1; PID:98824  
C;Superfamily: delta-4 protein; EGF homology  
F;299-332/Domain: EGF homology <EGX1>  
F;339-370/Domain: EGF homology <EGF1>  
F;416-447/Domain: EGF homology <EGX2>  
F;454-485/Domain: EGF homology <EGF>  
F;492-523/Domain: EGF homology <EGF3>

Query Match 41.9%; Score 388; DB 2; Length 728;  
Best Local Similarity 49.7%; Pred. No. 7.2e-30;  
Matches 87; Conservative 15; Mismatches 27; Indels 46; Gaps 5;

Qy 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60

Db 597 TMNLANCQREKDISVIGATQIKNTNKKVDFH--SDNSKNGY-KVRYPSVDYNLVHE 653

Qy 61 LKGDPTAVRTSHSKRDTKCQSPGSGRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 120

Db 654 LKNED-SVKEEHGKCEAKCETYDSAEKS-----AVQ 685

Qy 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175

Db 686 LK-----SSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIA 725

RESULT 3

JC7570  
Delta-4 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: JC7570  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J. Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.  
A;Reference number: JC7569; MUID: 21064937; PMID:11134954  
A;Accession: JC7570  
A;Molecule type: mRNA  
A;Residues: 1-685 <YON>  
A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894  
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re  
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.  
C;Genetics:  
A;Gene: delta-4  
C;Superfamily: delta-4 protein; EGF homology  
C;Keywords: transmembrane protein

Query Match 13.7%; Score 126.5; DB 2; Length 685;  
Best Local Similarity 26.7%; Pred. No. 0.0002;  
Matches 47; Conservative 23; Mismatches 43; Indels 63; Gaps 7;

Qy 2 MNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQDL 61

Db 568 MNLSDFQKD-----NLIPAAQLKNTNQKKELEV-DCGLDKSNCGKQQNHTLDYNL---- 617

Qy 62 KGDPTAVRTSHSKRDTKCQSPGSSGR--RRGPRPHSGXACCGPGSGGTGWGVSSWNHCSV 119

Db 618 -----APGDLGRGTMPGKFPKSHDKSL-----GEKAPLRLHS 648

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175

Db 649 EKPEC-----RISAICS-PRDSMYQSVCLISEERNECVIA 682

RESULT 4

JC7569  
Delta-4 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: JC7569  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J. Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A;Reference number: JC7569; MUID: 21064937; PMID:11134954

A;Accession: JC7569

A;Molecule type: mRNA

A;Residues: 1-686 <YON>

A;Cross-references: UNIPROT:Q9DBU9; DDBJ:AB043893

C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re  
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.

C;Genetics:

A;Gene: delta-4

C;Superfamily: delta-4 protein; EGF homology

Query Match 13.6%; Score 125.5; DB 2; Length 686;

Best Local Similarity 24.9%; Pred. No. 0.00025;

Matches 44; Conservative 25; Mismatches 43; Indels 65; Gaps 6;

Qy 2 MNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQDL 61

Db 569 MNLSDFQKD-----NLIPAAQLKNTNQKKELEV-DCGLDKSNCGKQLQNHTLDYNLAPGL 622

Qy 62 KGDPTAVRTSHSKRDTKCQSPGSSGRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVSL 121

Db 623 LG-----RGGMPGKYPHSDKS-----LGEKV 643

Qy 122 PKCSHAFIVDFLYFPFSGEASERKRPD---SGCSTSKDTKYQSVYVISEEKDECVIA 175

Db 644 PRLHS-----EKPECRISAICSPRDSMYQSVCLISEERNECVIA 683

RESULT 5

TVHUGL  
transforming protein gli - human  
N;Alternate names: glioma-associated transforming protein  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: S00672  
R;Kinzler, K.W.; Ruppert, J.M.; Bigner, S.H.; Vogelstein, B. Nature 332, 371-374, 1988  
A;Title: The GLI gene is a member of the Kruppel family of zinc finger proteins.  
A;Reference number: S00672; MUID:88175051; PMID:2832761  
A;Accession: S00672  
A;Molecule type: mRNA  
A;Residues: 1-1106 <KIN>  
A;Cross-references: UNIPROT:P08151; EMBL:X07384; NID:G31767; PIDN:CAA30297.1; PID:G31768  
C;Genetics:  
A;Gene: GDB:GLI  
A;Cross-references: GDB:119988; OMIM:165220  
A;Map position: 12q13.2-12q13.3  
C;Superfamily: gli transforming protein  
C;Keywords: DNA binding; duplication; oncogene; transcription regulation; transforming p  
F;235-260/Region: zinc finger CCHH motif  
F;268-295/Region: zinc finger CCHH motif  
F;301-325/Region: zinc finger CCHH motif  
F;331-356/Region: zinc finger CCHH motif  
F;362-387/Region: zinc finger CCHH motif

Query Match 9.6%; Score 88.5; DB 1; Length 1106;

Best Local Similarity 21.8%; Pred. No. 1.7;

Matches 42; Conservative 24; Mismatches 62; Indels 65; Gaps 8;

Qy 39 SSDKNGFQKARYPSVDYNLVQDLKGD-DTAVRTSHSKR----DTKCQSPGSS----- 85

Db 69 SSPRSAVKLTKKRALSISPLSDASLDLQTVIRTSPSSLVAFINSRCTSPGGSYGHLISGT 128

Qy 86 -----GRRRGPRPHSGXACCGP-GSGGGTGWGVSSWNHCSVSLPKCSHAFIVDFL 133

Db 129 MSPSLGFPPAQMNHQKGFSPFVGVPQCGPHDSARG--GMIPHPQSRGPFPTCQLKSELDM 186

Qy 134 Y-----FPFSGEAS-----ERKRPDS-----GCSTSK 155

Db 187 VGKREEPLEGDMSSPNSTGIQDPLLGLMLDGRDLEREKREPESVYETDCRWDGCSQEF 246

Qy 156 DTKYQSVYVISEE 168









Query Match 8.5%; Score 78.5; DB 2; Length 512;  
Best Local Similarity 26.2%; Pred. No. 7.1;  
Matches 32; Conservative 7; Mismatches 54; Indels 29; Gaps 4;  
  
QY 12 KDISVSIIGATGIXNTNKKADPXXGDXSSDKNGFQKARYPSVDYNLVQDLKGDDTAVRTS 71  
Db 72 KDIRVD--DRVGFQNHNNLSITNADKSSDRNSGKMMSYLG-----RTK 113  
  
QY 72 HSKRDTKCQSPGSSGRRRGPRPHSGXACCGPGSGGTGCVSSWNHCS-----VSLPKC 124  
Db 114 SSDNDSISQCSSVHHHERACSSHSGE----DGSFGAAWRQNSLSQGGLVTASPLVGLPEI 169  
  
QY 125 SH 126  
Db 170 SH 171  
  
RESULT 14  
T49418  
hypothetical protein B1D4.330 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: T49418  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25022  
A;Accession: T49418  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-538 <SCH>  
A;Cross-references: UNIPROT:Q9P649; EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.330  
A;Experimental source: BAC clone B1D4; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B1D4.330  
A;Map position: 6  
A;Introns: 162/2

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Best Local Similarity 24.0%; Pred. No. 9.3;  
Matches 35; Conservative 18; Mismatches 48; Indels 45; Gaps 9;  
  
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Db 95 QHAQYQ--HYHAV---TGDNKKATTKRAKHGP-EAPGGEGRKFACPFQCHNPARYRTVK 148  
  
QY 98 ACCGPGSGGGTGWV-----SSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERK 145  
Db 149 TCCGPG-----WDSVHRVKEHIYRRHSLKNTC----PRCYDQFKTD-----DDLKRHQ 192  
  
QY 146 RPDSGCSTSKDTKYQSVYVISEEKDE 171  
Db 193 RAETPCRLRKDNVPE---VITDEQDK 215

RESULT 15  
C96623  
hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C96623  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: C96623  
A;Status: preliminary

A;Molecule type: DNA  
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A;Cross-references: UNIPROT:Q9XIE0; GB:AE005173; NID:g5080823; PIDN:AAD39332.1; GSPDB:GN  
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Best Local Similarity 32.6%; Pred. No. 16;  
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QY 36 GDXSSDKNGFQKARYPSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRRGPRPHS 95  
Db 103 GDKSGD--GFRRTGADQDDNDGDDEVGDE-SIEEAFSFHVKKSQSASSSGGEIRDQSN 159  
  
QY 96 GXACCGPGSGGTGCVSSWNHCSVSLPKCSHA 127  
Db 160 GGGGGGGGGGGGRYTTSS--SASPSRPSSSSA 189

Search completed: December 2, 2004, 04:02:06  
Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 04:01:28 ; Search time 3243 Seconds  
(without alignments)  
19.244 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926  
Sequence: 1 TMNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	916	98.9	175	9 US-09-908-322-23	Sequence 23, Appl
2	916	98.9	175	10 US-09-783-931-23	Sequence 23, Appl
3	631.5	68.2	118	9 US-09-908-322-17	Sequence 17, Appl
4	631.5	68.2	118	10 US-09-783-931-17	Sequence 17, Appl
5	527.5	57.0	702	9 US-09-995-593A-4	Sequence 4, Appli
6	527.5	57.0	723	9 US-09-828-366-21	Sequence 21, Appl
7	527.5	57.0	723	9 US-09-995-593A-9	Sequence 9, Appli
8	527.5	57.0	723	14 US-10-028-072-346	Sequence 346, App
9	527.5	57.0	723	14 US-10-140-808-346	Sequence 346, App
10	527.5	57.0	723	14 US-10-121-049-346	Sequence 346, App
11	527.5	57.0	723	14 US-10-123-904-346	Sequence 346, App
12	527.5	57.0	723	14 US-10-140-470-346	Sequence 346, App
13	527.5	57.0	723	14 US-10-175-746-346	Sequence 346, App

14	527.5	57.0	723	14	US-10-176-918-346	Sequence 346, App
15	527.5	57.0	723	14	US-10-176-921-346	Sequence 346, App
16	527.5	57.0	723	14	US-10-137-865-346	Sequence 346, App
17	527.5	57.0	723	14	US-10-140-474-346	Sequence 346, App
18	527.5	57.0	723	14	US-10-142-431-346	Sequence 346, App
19	527.5	57.0	723	14	US-10-143-114-346	Sequence 346, App
20	527.5	57.0	723	14	US-10-140-002-346	Sequence 346, App
21	527.5	57.0	723	14	US-10-142-419-346	Sequence 346, App
22	527.5	57.0	723	14	US-10-241-476-27	Sequence 27, Appl
23	527.5	57.0	723	14	US-10-123-262-346	Sequence 346, App
24	527.5	57.0	723	14	US-10-142-423-346	Sequence 346, App
25	527.5	57.0	723	14	US-10-121-050-346	Sequence 346, App
26	527.5	57.0	723	14	US-10-141-755-346	Sequence 346, App
27	527.5	57.0	723	14	US-10-143-032-346	Sequence 346, App
28	527.5	57.0	723	14	US-10-123-108-346	Sequence 346, App
29	527.5	57.0	723	14	US-10-123-236-346	Sequence 346, App
30	527.5	57.0	723	14	US-10-123-261-346	Sequence 346, App
31	527.5	57.0	723	14	US-10-140-921-346	Sequence 346, App
32	527.5	57.0	723	14	US-10-140-928-346	Sequence 346, App
33	527.5	57.0	723	14	US-10-121-045-346	Sequence 346, App
34	527.5	57.0	723	14	US-10-123-292-346	Sequence 346, App
35	527.5	57.0	723	14	US-10-123-903-346	Sequence 346, App
36	527.5	57.0	723	14	US-10-124-819-346	Sequence 346, App
37	527.5	57.0	723	14	US-10-124-822-346	Sequence 346, App
38	527.5	57.0	723	14	US-10-140-925-346	Sequence 346, App
39	527.5	57.0	723	14	US-10-160-498-346	Sequence 346, App
40	527.5	57.0	723	14	US-10-124-824-346	Sequence 346, App
41	527.5	57.0	723	14	US-10-127-825A-346	Sequence 346, App
42	527.5	57.0	723	14	US-10-127-829A-346	Sequence 346, App
43	527.5	57.0	723	14	US-10-127-835A-346	Sequence 346, App
44	527.5	57.0	723	14	US-10-127-839A-346	Sequence 346, App
45	527.5	57.0	723	14	US-10-127-901A-346	Sequence 346, App

ALIGNMENTS

RESULT 1

US-09-908-322-23

; Sequence 23, Application US/09908322

; Patent No. US20020107194A1

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA: US/09/908,322

; FILING DATE: 17-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/981,392

; FILING DATE: 22-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 7326-123





US-09-908-322-17

Query Match 68.2%; Score 631.5; DB 9; Length 118;  
Best Local Similarity 99.2%; Pred. No. 3.8e-57;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 57 LVQDLKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGGTGWGVSSWNH 116  
Db 1 LVQDLKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGGTGWGVSSW-H 59

QY 117 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 175  
Db 60 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 118

RESULT 4

US-09-783-931-17  
; Sequence 17, Application US/09783931  
; Publication No. US20030073620A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; AND FRAGMENTS  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/783,931  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-783-931-17

Query Match 68.2%; Score 631.5; DB 10; Length 118;  
Best Local Similarity 99.2%; Pred. No. 3.8e-57;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 57 LVQDLKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGGTGWGVSSWNH 116  
Db 1 LVQDLKGGDTAVRTSHSKRDTKCQSPGSSGRRRGRPHSGXACCGPGSGGGTGWGVSSW-H 59

QY 117 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 175  
Db 60 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 118

RESULT 5

US-09-995-593A-4  
; Sequence 4, Application US/09995593A  
; Patent No. US20020128197A1  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP8447DIV  
; CURRENT APPLICATION NUMBER: US/09/995,593A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 09/068,740  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 702  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-995-593A-4

Query Match 57.0%; Score 527.5; DB 9; Length 702;  
Best Local Similarity 64.8%; Pred. No. 1.8e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFXGXSSDKNGFQKARYPSVDYNLVQD 60  
Db 568 TMNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 625

QY 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 119  
Db 626 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 662

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 175  
Db 663 -----GEASERKRPDSGCSTSKDTKYQSVVYVISEEKDECVIA 699

RESULT 6

US-09-828-366-21  
; Sequence 21, Application US/09828366  
; Patent No. US20020010137A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klein, Robert D.  
; APPLICANT: Napier, Mary  
; APPLICANT: Wood, William I.  
; APPLICANT: Yuan, Jean  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
; CELL GROWTH  
; FILE REFERENCE: P1694R1C1  
; CURRENT APPLICATION NUMBER: US/09/828,366  
; CURRENT FILING DATE: 2001-04-05  
; Prior filing data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 21  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapien



;  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/064809  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065846  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/066453  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/069212  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069278  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069334  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069694  
; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/072320  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: 60/073612  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081695  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 60/081817  
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; PRIOR APPLICATION NUMBER: 60/081818  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-24  
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; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085149  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13

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; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/086414  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/086430  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088730  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088741  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088810  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088858  
; PRIOR FILING DATE: 19/98-06-11  
; PRIOR APPLICATION NUMBER: 60/089532  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089599  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
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; PRIOR APPLICATION NUMBER: 60/090538  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07

Query Match 57.0%; Score 527.5; DB 14; Length 723;

Best Local Similarity 64.8%; Pred. No. 1.8e-45;

Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy	1	TMNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD	60
Db	589	TMNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD	646
Qy	61	LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV	119
Db	647	LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPPTLRG-----	683
Qy	120	SLPKCSHAFTVDLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA	175
Db	684	-----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA	720

RESULT 9

US-10-140-808-346  
; Sequence 346, Application US/10140808  
; Publication No. US20030017563A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 589 TMNNLANCQREKDISVSIIGATGIXNTNKKADF-HGDHSAADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 647 LKGGDDTAVRDAHSKRDTKCQPOGSSGEEKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
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Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720

RESULT 10
US-10-121-049-346
; Sequence 346, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
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Db 589 TMNNLANCQREKDISVSIIGATGIXNTNKKADF-HGDHSAADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
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Db 647 LKGGDDTAVRDAHSKRDTKCQPOGSSGEEKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
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Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720
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RESULT 10
US-10-121-049-346
; Sequence 346, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
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; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 589 TMNNLANCQREKDISVSIIGATGIXNTNKKADF-HGDHSAADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 647 LKGGDDTAVRDAHSKRDTKCQPOGSSGEEKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720

RESULT 11
US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 589 TMNNLANCQREKDISVSIIGATGIXNTNKKADF-HGDHSAADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 647 LKGGDDTAVRDAHSKRDTKCQPOGSSGEEKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720
```

```
RESULT 11
US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
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```
RESULT 12
US-10-140-470-346
; Sequence 346, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY      1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY      61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      647 LKGGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG-----683

QY      120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      684 -----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 720

RESULT 13
US-10-175-746-346
; Sequence 346, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY      1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY      61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      647 LKGGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG-----683

QY      120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      684 -----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 720

RESULT 14
US-10-176-918-346
; Sequence 346, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY      1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY      61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      647 LKGGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG-----683

QY      120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      684 -----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 720
```



```
Db      589  TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
Qy      61   LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
         |||||||:|||||:|||||:|
Db      647  LKGGDTAVRDAHSKRDTKCQPGQSSGEEKGTPTTLRG----- 683
Qy      120  SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
         |||||||:|||||:|||||:|
Db      684  -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720
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```
RESULT 15
US-10-176-921-346
; Sequence 346, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-346
```

```
Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy      1   TMNNLANCQREKDISVSIIGATQIKNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
         |||||||:|||||:|||||:|
Db      589  TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
Qy      61   LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
         |||||||:|||||:|||||:|
Db      647  LKGGDTAVRDAHSKRDTKCQPGQSSGEEKGTPTTLRG----- 683
Qy      120  SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
         |||||||:|||||:|||||:|
Db      684  -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 03:51:27 ; Search time 153 Seconds  
(without alignments)  
410.311 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	Length	DB	ID	Description
1	908	98.1	175	2	AAW11724	Aaw11724	H-Delta-1
2	678.5	73.3	175	2	AAW11721	Aaw11721	H-Delta-1
3	527.5	57.0	702	2	AAW18349	Aaw18349	Prolifera
4	527.5	57.0	702	2	AAW75495	Aaw75495	Truncated
5	527.5	57.0	723	2	AAW18353	Aaw18353	Prolifera
6	527.5	57.0	723	2	AAW75492	Aaw75492	Human del
7	527.5	57.0	723	2	AAW94498	Aaw94498	Human del
8	527.5	57.0	723	3	AAW83227	Aay83227	PRO172 po
9	527.5	57.0	723	3	AAB33422	Aab33422	Human PRO
10	527.5	57.0	723	3	AAB24388	Aab24388	Human PRO
11	527.5	57.0	723	3	AAW79032	Aay79032	Human del
12	527.5	57.0	723	3	AAB00172	Aab00172	PRO172 po
13	527.5	57.0	723	4	AAU12344	Aau12344	Human PRO
14	527.5	57.0	723	4	AAB53064	Aab53064	Human ang
15	527.5	57.0	723	6	ABO17788	Abu17788	Novel hum
16	527.5	57.0	723	6	ABU81042	Abu81042	Human PRO
17	527.5	57.0	723	6	ABP97824	Abp97824	Amino aci
18	527.5	57.0	723	6	ABU66742	Abu66742	Human PRO
19	527.5	57.0	723	6	ABU55879	Abu55879	Human not
20	527.5	57.0	723	6	AAE34035	Aae34035	Human not
21	527.5	57.0	723	6	ABU59823	Abu59823	Novel sec
22	527.5	57.0	723	6	ABO25013	Abu25013	Human sec
23	527.5	57.0	723	6	ABP72566	Abp72566	Human Not
24	527.5	57.0	723	6	ABU67018	Abu67018	Human sec
25	527.5	57.0	723	6	ADA45865	Ada45865	Novel hum

26	527.5	57.0	723	6	ADA76296	Ada76296	Human PRO
27	527.5	57.0	723	6	ADA18946	Ada18946	Human PRO
28	527.5	57.0	723	6	ADA61569	Ada61569	Homo eapi
29	527.5	57.0	723	6	ADB19354	Adb19354	Novel hum
30	527.5	57.0	723	6	ADB27895	Adb27895	Human PRO
31	527.5	57.0	723	6	ADA86374	Ada86374	Novel hum
32	527.5	57.0	723	6	ADB15938	Adb15938	Human PRO
33	527.5	57.0	723	6	ADA47724	Ada47724	Human PRO
34	527.5	57.0	723	6	ADA67519	Ada67519	Human PRO
35	527.5	57.0	723	6	ADB30526	Adb30526	Human PRO
36	527.5	57.0	723	6	ADA85822	Ada85822	Novel hum
37	527.5	57.0	723	6	ADA97034	Ada97034	Human PRO
38	527.5	57.0	723	6	ADA79338	Ada79338	Human PRO
39	527.5	57.0	723	6	ADA87477	Ada87477	Novel hum
40	527.5	57.0	723	6	ADB16679	Adb16679	Human PRO
41	527.5	57.0	723	6	ADA91771	Ada91771	Novel hum
42	527.5	57.0	723	6	ADB14834	Adb14834	Human PRO
43	527.5	57.0	723	6	ADB18795	Adb18795	Novel hum
44	527.5	57.0	723	6	ADA94010	Ada94010	Human PRO
45	527.5	57.0	723	6	ADB19906	Adb19906	Novel hum

ALIGNMENTS

RESULT 1  
AAW11724  
ID AAW11724 standard; protein; 175 AA.  
XX  
AC AAW11724;  
XX  
DT 28-APR-1997 (first entry)  
XX  
DE H-Delta-1 polypeptide predicted sequence.  
XX  
KW H-Delta-1; cell proliferation; nervous system disorder;  
KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;  
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 25 /note= "undetermined amino acid residue"  
FT Misc-difference 34 /note= "undetermined amino acid residue"  
FT Misc-difference 35 /note= "undetermined amino acid residue"  
FT Misc-difference 38 /note= "undetermined amino acid residue"  
FT Misc-difference 97 /note= "undetermined amino acid residue"  
WO9701571-A1.  
16-JAN-1997.  
28-JUN-1996; 96WO-US011178.  
28-JUN-1995; 95US-0000589P.  
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
(UYVA ) UNIV YALE.  
Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;  
Gray GE;  
WPI; 1997-100159/09.  
N-PSDB; AAT58900.  
New vertebrate Delta protein, DNA and antibodies - for treating and  
preventing cancer, nervous system disorders and for tissue regeneration.



KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
XX Homo sapiens.  
OS WO9719172-A1.  
XX PD 29-MAY-1997.  
XX PF 15-NOV-1996; 96WO-JP003356.  
XX PR 17-NOV-1995; 95JP-00299611.  
XX PR 30-NOV-1995; 95JP-00311811.  
XX PA (ASAH ) ASAH KASEI KOGYO KK.  
XX PI Sakano S, Itoh A;  
XX DR WPI; 1997-298110/27.  
XX PT Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress  
PT proliferation and differentiation of undifferentiated human blood cells.  
XX PS Claim 4; Page 61-64; 114pp; Japanese.  
XX CC The present sequence represents a polypeptide which suppresses  
CC proliferation and differentiation of undifferentiated cells such as  
CC neurons and blood cells. The polypeptide may be used for the prevention  
CC and control of disorders involving undifferentiated cells, such as  
CC leukaemia and malignant tumours, and improvement of blood formation, e.g.  
CC after immunosuppression  
XX SQ Sequence 702 AA;  
Query Match 57.0%; Score 527.5; DB 2; Length 702;  
Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60  
Db 568 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 625  
QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
Db 626 LKGGDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 662  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175  
Db 663 -----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 699  
RESULT 4  
AAW75495  
ID AAW75495 standard; protein; 702 AA.  
XX AC AAW75495;  
XX DT 27-APR-1999 (first entry)  
XX DE Truncated human delta-1 protein #3.  
XX KW Human; delta-1 protein; ligand; notch; drug; vascular cell; primer; PCR;  
KW amplification; truncation.  
XX OS Homo sapiens.  
XX PN JP10316582-A.  
XX PD 02-DEC-1998.  
XX PF 14-MAY-1997; 97JP-00124062.  
XX PR 14-MAY-1997; 97JP-00124062.

PA (ASAH ) ASAH KASEI KOGYO KK.  
XX WPI; 1999-076401/07.  
XX PT Vascular cell controlling agent comprises polypeptide - which is human  
PT notch ligand and is used as drug.  
XX PS Claim 2; Page 14-16; 21pp; Japanese.  
XX CC This sequence represents a truncated human delta-1 protein corresponding  
CC to amino acids 1-702 of the mature protein (see AAW75492). The delta-1  
CC protein is a ligand of the human notch protein and the protein or  
CC fragments, especially AAW75493-W75495, can be used as a drug to control  
CC vascular cells. The sequences were isolated and the truncated fragments  
CC were generated using the primers AAX16818-X16831  
XX SQ Sequence 702 AA;  
Query Match 57.0%; Score 527.5; DB 2; Length 702;  
Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60  
Db 568 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 625  
QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
Db 626 LKGGDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 662  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175  
Db 663 -----GEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 699  
RESULT 5  
AAW18353  
ID AAW18353 standard; protein; 723 AA.  
XX AC AAW18353;  
XX DT 11-FEB-1998 (first entry)  
XX DE Proliferation and differentiation suppression polypeptide.  
XX KW Proliferation; differentiation; suppression; human; delta-1; serrate-1;  
KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /label= Signal  
FT Protein 22..723  
FT /label= Differentiation\_suppression\_protein  
XX PN WO9719172-A1.  
XX PD 29-MAY-1997.  
XX PF 15-NOV-1996; 96WO-JP003356.  
XX PR 17-NOV-1995; 95JP-00299611.  
XX PR 30-NOV-1995; 95JP-00311811.  
XX PA (ASAH ) ASAH KASEI KOGYO KK.  
XX PI Sakano S, Itoh A;  
XX DR WPI; 1997-298110/27.  
XX DR N-ESDB; AAT70174.  
XX PT Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress





XX										
SQ	Sequence 723 AA;									
Query Match 57.0%; Score 527.5; DB 2; Length 723;										
Best Local Similarity 64.8%; Pred. No. 1.6e-45;										
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4										
QY	1	TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD	60							
Db	589	TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSDAKNGF-KARYPAVDYNLVQD	646							
QY	61	LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV	119							
Db	647	LKGDDTAVRDAHSKRDTKCQPGSSGEEKGPTTLRG-----	683							
QY	120	SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA	175							
Db	684	-----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA	720							
RESULT 8										
AAY83227										
ID	AAY83227 standard; protein; 723 AA.									
XX	AAY83227;									
AC	16-AUG-2000 (first entry)									
DT	PRO172 Polypeptide.									
XX	Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;									
KW	uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;									
KW	leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.									
XX	Homo sapiens.									
OS										
XX										
FH	Key									
FT	Peptide									
FT	1. .21									
FT	/label= Signal_peptide									
FT	Modified-site									
FT	2. .8									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	37. .43									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	40. .46									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	93. .97									
FT	/note= "Casein kinase II phosphorylation site"									
FT	Modified-site									
FT	98. .104									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	99. .105									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	131. .135									
FT	/note= "Casein kinase II phosphorylation site"									
FT	Modified-site									
FT	154. .158									
FT	/note= "Casein kinase II phosphorylation"									
FT	Modified-site									
FT	176. .185									
FT	/note= "Tyrosine kinase phosphorylation site"									
FT	Modified-site									
FT	203. .207									
FT	/note= "Casein kinase II phosphorylation site"									
FT	Domain									
FT	243. .255									
FT	/label= EGF-like_domain									
FT	Modified-site									
FT	252. .261									
FT	/note= "Tyrosine kinase phosphorylation site"									
FT	Modified-site									
FT	262. .268									
FT	/note= "N-myristoylation site"									
FT	Domain									
FT	274. .286									
FT	/note= "EGF-like domain"									
FT	Modified-site									
FT	281. .287									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	282. .288									
FT	/note= "N-myristoylation site"									
FT	Modified-site									
FT	301. .307									
FT	/note= "N-myristoylation site"									
FT										

FT	Modified-site	310. .316	/note= "N-myristoylation site"
FT		314. .326	
FT	Domain	/label= EGF-like_domain	
FT		328. .334	
FT	Modified-site	/note= "N-myristoylation domain"	
FT		340. .346	
FT	Modified-site	/note= "N-myristoylation site"	
FT		342. .346	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		343. .355	
FT	Modified-site	/note= "Asn and Asp hydroxylation site"	
FT		344. .348	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		352. .364	
FT	Domain	/label= EGF-like_domain	
FT		369. .373	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		378. .384	
FT	Modified-site	/note= "N-myristoylation site"	
FT		387. .393	
FT	Modified-site	/note= "N-myristoylation site"	
FT		391. .403	
FT	Domain	/label= EGF-like_domain	
FT		420. .432	
FT	Modified-site	/note= "Asn and Asp hydroxylation site"	
FT		429. .441	
FT	Domain	/label= EGF-like_domain	
FT		457. .461	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		458. .480	
FT	Modified-site	/label= Asn and Asp hydroxylation site	
FT		467. .479	
FT	Domain	/label= EGF-like_domain	
FT		477. .481	
FT	Modified-site	/note= "N-glycosylation site"	
FT		483. .487	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		495. .499	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		505. .517	
FT	Domain	/label= EGF-like_domain	
FT		512. .518	
FT	Modified-site	/note= "N-myristoylation site"	
FT		548. .568	
FT	Domain	/label= Transmembrane_domain	
FT		552. .563	
FT	Binding-site	/label= Prokaryotic membrane lipoprotein lipid site	
FT		659. .663	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		660. .664	
FT	Modified-site	/note= "cAMP and cGMP dependent protein kinase phosphorylation site"	
FT		670. .674	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		671. .675	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT		676. .682	
FT	Modified-site	/note= "N-myristoylation site"	
FT		683. .689	
FT	Modified-site	/note= "N-myristoylation site"	
FT		695. .701	
FT	Modified-site	/note= "N-myristoylation site"	
FT		698. .702	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
XX			
PN	WO200021996-A2.		
XX			
PD	20-APR-2000.		
XX			
PF	05-OCT-1999;	99WO-US023089.	
XX			



CC represent human PRO polynucleotide and protein sequences given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFFXXGDXSSDKNGFQKARYPSVDYNLVQD 60  
|||  
Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
|||  
Db 647 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIA 175  
|||  
Db 684 -----GEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIA 720

RESULT 10  
AAB24388  
ID AAB24388 standard; protein; 723 AA.  
XX  
AC AAB24388;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human PRO172 protein sequence SEQ ID NO:4.  
XX  
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200032221-A2.  
XX  
PD 08-JUN-2000.  
XX  
PF 30-NOV-1999; 99WO-US028313.  
XX

01-DEC-1998; 98WO-US025108.  
PR 16-DEC-1998; 98US-0112850P.  
PR 12-JAN-1999; 99US-0115554P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-OCT-1999; 99US-0162506P.  
XX

(GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;  
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;  
PI Smith V, Watanabe CK, Williams PM, Wood WT;  
XX  
XX WPI; 2000-412154/35.  
DR N-PSDB; AAB24388.  
XX

PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing  
PT and treating diagnosing a cardiovascular, endothelial or angiogenic  
PT disorders in mammals.  
XX  
PS Claim 72; Fig 2; 315pp; English.  
XX  
CC The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating disorder in mammals a  
CC cardiovascular, endothelial or angiogenic disorder in mammals by  
CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
CC and for identifying agonists and antagonists of these processes. The  
CC nucleic acids and the proteins they encode may be used in the prevention,  
CC treatment and diagnosis of diseases associated with inappropriate PRO  
CC expression such as cardiovascular, endothelial or angiogenic disorders in  
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For  
CC example, the nucleic acids (NCs) and vectors containing them and the PRO  
CC polypeptide may be used to treat disorders associated with decreased PRO  
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent  
CC nucleotide and protein sequences used in the exemplification of the  
CC present invention  
XX  
SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFFXXGDXSSDKNGFQKARYPSVDYNLVQD 60  
|||  
Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
|||  
Db 647 LKGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIA 175  
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Db 684 -----GEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIA 720

RESULT 11  
AAY79032  
ID AAY79032 standard; protein; 723 AA.  
XX  
AC AAY79032;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Human delta protein amino acid sequence.  
XX  
KW Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;  
KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;  
KW tissue regeneration; liver cirrhosis; keloid formation; baldness;  
KW inner ear disorder; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200002897-A2.  
XX  
PD 20-JAN-2000.  
XX  
PF 13-JUL-1999; 99WO-US015817.  
XX  
PR 13-JUL-1998; 98US-0092513P.  
PR 19-OCT-1998; 98US-0104834P.  
XX

(UYVA ) UNIV YALE.  
XX  
PI Artavanis-Tsakonas S, Rand MD, Qi H;  
XX  
XX WPI; 2000-282852/24.  
DR N-PSDB; AAZ98679.  
XX





FT Domain 467. .479  
FT /label= EGF-like domain cysteine pattern signatu  
FT Modified-site 477. .481  
FT /note= "N-glycosylation site"  
FT Modified-site 483. .487  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 495. .499  
FT /note= "Casein kinase II phosphorylation site"  
FT Domain 505. .517  
FT /label= EGF-like domain cysteine pattern signatu  
FT Modified-site 512. .518  
FT /note= "N-myristoylation site"  
FT Domain 548. .568  
FT /label= Transmembrane domain  
FT Binding-site 552. .563  
FT /label= Prokaryotic membrane lipoprotein lipid a  
FT Modified-site 659. .663  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 660. .664  
FT /note= "cAMP- and cGMP-dependent protein kinase  
FT phosphorylation site"  
FT Modified-site 670. .674  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 671. .675  
FT /note= "Casein kinase phosphorylation site"  
FT Modified-site 676. .682  
FT /note= "N-myristoylation site"  
FT Modified-site 683. .689  
FT /note= "N-myristoylation site"  
FT Modified-site 695. .701  
FT /note= "N-myristoylation site"  
FT Modified-site 698. .702  
FT /note= "Casein kinase II phosphorylation site"  
XX  
PN WO200055319-A1.  
XX  
XX 21-SEP-2000.  
PD  
XX 02-DEC-1999; 99WO-US028564.  
XX  
PR 12-MAR-1999; 99US-0123957P.  
PR 28-APR-1999; 99US-0131445P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 08-SEP-1999; 99WO-US020594.  
PR 15-SEP-1999; 99WO-US021090.  
PR 05-OCT-1999; 99WO-US023089.  
PR 30-NOV-1999; 99WO-US028313.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;  
PI Yuan J;  
XX  
DR WPI; 2000-638201/61.  
DR N-PSDB; AAA54105.  
XX  
PT PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for  
PT treating tumors including cancers of the breast and lung, leukemia and  
PT for identifying compounds capable of inhibiting growth of neoplastic  
PT cells.  
XX  
PS Claim 31; Fig 8; 133pp; English.  
XX  
CC Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their  
CC agonists (preferably anti-PRO agonist antibody or a small molecule  
CC mimicking the biological activity of PRO polypeptide) are useful in vitro  
CC or in vivo for inhibiting the growth of a tumour cell. Compositions  
CC comprising the PRO polypeptides are useful for inhibiting neoplastic cell  
CC growth and for treating cancer including breast, ovarian, renal,  
CC colorectal, uterine, prostate, lung, bladder, central nervous system  
CC cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also  
CC useful for treating other disorders such as neuronal, glial, astrocytal,

CC hypothalamic and other glandular, macrophagal, epithelial, stromal,  
CC blastocoelic disorders and inflammatory, angiogenic and immunologic  
CC disorders as well as being useful for identifying agonists to PRO  
CC polypeptides by contacting the polypeptide with a candidate molecule and  
CC monitoring biological activity mediated by the polypeptide  
XX  
SQ Sequence 723 AA;  
Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60  
DB 589 TMNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646  
QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
DB 647 LKGGDDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKECVIA 175  
DB 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKECVIA 720  
RESULT 13  
AAU12344  
ID AAU12344 standard; protein; 723 AA.  
XX  
AC AAU12344;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human PRO172 polypeptide sequence.  
XX  
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
KW A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200140466-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 01-DEC-2000; 2000WO-US032678.  
XX  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.





```
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to screen
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
CC therapy. PRO nucleic acids can also be used to produce transgenic animals
CC useful for the development and screening of potential therapeutic agents.
CC The present sequence represents a PRO protein of the invention
XX
SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.6e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSPKNGFQKARYPSVDYNLVQD 60
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
589 TMNNLANCQREKDISVSIIGATGIXNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGGDTAVRTSHSKRDTKCQSGSSGRRRG-PRPHSGXACCPGSGGTTGWSSMNHCSV 119
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
647 LKGGDTAVRDAHSKRDTKCQPGSSGEEKGTPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720

RESULT 15
ABO17788
ID ABO17788 standard; protein; 723 AA.
XX
AC ABO17788;
XX
XX 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO172.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
XX US2003032156-A1.
PN
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
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